

SEQUENCE LISTING

<110> MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;

OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji

<120> A process for producing isoprenoid compounds by microorganisms and
a method for screening compounds with antibiotic or weeding activity

<130>

<140> PCT/JP99/01987

<141> 1999-04-14

<150> JP98/103101

<151> 1998-04-14

<150> JP98/221910

<151> 1998-08-05

<150> JP99/035739

<151> 1999-02-15

<160> 34

<170> PatentIn Ver. 2.0

<210> 1

<211> 620

<212> PRT

<213> Escherichia coli

<400> 1

Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
1 5 10 15

Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
20 25 30

Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
35 40 45

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
50 55 60

Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
65 70 75 80

Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
85 90 95

Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
100 105 110

Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
115 120 125

Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
130 135 140

Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
145 150 155 160

Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
165 170 175

Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
180 185 190

Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
195 200 205

Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
210 215 220

Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
225 230 235 240

Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
245 250 255

His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
260 265 270

Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
275 280 285

Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
290 295 300

Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
305 310 315 320

Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
325 330 335

Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met

340	345	350
Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile		
355	360	365
Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly		
370	375	380
Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr		
385	390	395
Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe		
405	410	415
Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln		
420	425	430
Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile		
435	440	445
Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly		
450	455	460
Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn		
465	470	475
Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys		
485	490	495
Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly		
500	505	510

Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
515 520 525

Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu
530 535 540

Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala
545 550 555 560

Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His
565 570 575

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile
580 585 590

Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala
595 600 605

Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala
610 615 620

<210> 2

<211> 299

<212> PRT

<213> Escherichia coli

<400> 2

Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln
1 5 10 15

Ala Leu Ser Arg Phe Ile Ala Pro Leu Pro Phe Gln Asn Thr Pro Val

	20		25		30										
Val	Glu	Thr	Met	Gln	Tyr	Gly	Ala	Leu	Leu	Gly	Gly	Lys	Arg	Leu	Arg
	35		40		45										
Pro	Phe	Leu	Val	Tyr	Ala	Thr	Gly	His	Met	Phe	Gly	Val	Ser	Thr	Asn
	50		55		60										
Thr	Leu	Asp	Ala	Pro	Ala	Ala	Ala	Val	Glu	Cys	Ile	His	Ala	Tyr	Ser
	65		70		75		80								
Leu	Ile	His	Asp	Asp	Leu	Pro	Ala	Met	Asp	Asp	Asp	Asp	Leu	Arg	Arg
		85		90		95									
Gly	Leu	Pro	Thr	Cys	His	Val	Lys	Phe	Gly	Glu	Ala	Asn	Ala	Ile	Leu
	100		105		110										
Ala	Gly	Asp	Ala	Leu	Gln	Thr	Leu	Ala	Phe	Ser	Ile	Leu	Ser	Asp	Ala
	115		120		125										
Asp	Met	Pro	Glu	Val	Ser	Asp	Arg	Asp	Arg	Ile	Ser	Met	Ile	Ser	Glu
	130		135		140										
Leu	Ala	Ser	Ala	Ser	Gly	Ile	Ala	Gly	Met	Cys	Gly	Gly	Gln	Ala	Leu
	145		150		155		160								
Asp	Leu	Asp	Ala	Glu	Gly	Lys	His	Val	Pro	Leu	Asp	Ala	Leu	Glu	Arg
	165		170		175										
Ile	His	Arg	His	Lys	Thr	Gly	Ala	Leu	Ile	Arg	Ala	Ala	Val	Arg	Leu
	180		185		190										

Gly Ala Leu Ser Ala Gly Asp Lys Gly Arg Arg Ala Leu Pro Val Leu
195 200 205

Asp Lys Tyr Ala Glu Ser Ile Gly Leu Ala Phe Gln Val Gln Asp Asp
210 215 220

Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly
225 230 235 240

Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu
245 250 255

Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln
260 265 270

Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu
275 280 285

Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys
290 295

<210> 3

<211> 80

<212> PRT

<213> Escherichia coli

<400> 3

Met Pro Lys Lys Asn Glu Ala Pro Ala Ser Phe Glu Lys Ala Leu Ser
1 5 10 15

Glu Leu Glu Gln Ile Val Thr Arg Leu Glu Ser Gly Asp Leu Pro Leu

20

25

30

Glu Glu Ala Leu Asn Glu Phe Glu Arg Gly Val Gln Leu Ala Arg Gln

35

40

45

Gly Gln Ala Lys Leu Gln Gln Ala Glu Gln Arg Val Gln Ile Leu Leu

50

55

60

Ser Asp Asn Glu Asp Ala Ser Leu Thr Pro Phe Thr Pro Asp Asn Glu

65

70

75

80

<210> 4

<211> 348

<212> PRT

<213> Escherichia coli

<400> 4

Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr Cys Asn Leu Lys Tyr

1

5

10

15

Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr Asn Pro Leu Gly Lys

20

25

30

Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly Cys Met Thr Phe Gly

35

40

45

Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu Pro Glu Glu Ser Ser

50

55

60

Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly Ile Asn Phe Phe Asp

65

70

75

80

Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu Glu Ile Val Gly Arg

85

90

95

Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val Val Val Ala Thr Lys

100

105

110

Val Phe His Arg Val Gly Asp Leu Pro Glu Gly Leu Ser Arg Ala Gln

115

120

125

Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg Leu Gly Met Asp Tyr

130

135

140

Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr Asn Thr Pro Ile Glu

145

150

155

160

Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys Ala Gly Lys Ala Arg

165

170

175

Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln Phe Ala Gln Ala Leu

180

185

190

Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe Val Ser Met Gln Asp

195

200

205

His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg Glu Met Leu Pro Leu

210

215

220

Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp Ser Pro Leu Ala Arg

225

230

235

240

Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr Ala Arg Leu Val Ser

	245		250		255										
Asp	Glu	Val	Gly	Lys	Asn	Leu	Tyr	Lys	Glu	Ser	Asp	Glu	Asn	Asp	Ala
	260							265						270	
Gln	Ile	Ala	Glu	Arg	Leu	Thr	Gly	Val	Ser	Glu	Glu	Leu	Gly	Ala	Thr
	275						280						285		
Arg	Ala	Gln	Val	Ala	Leu	Ala	Trp	Leu	Leu	Ser	Lys	Pro	Gly	Ile	Ala
	290					295						300			
Ala	Pro	Ile	Ile	Gly	Thr	Ser	Arg	Glu	Glu	Gln	Leu	Asp	Glu	Leu	Leu
305					310					315				320	
Asn	Ala	Val	Asp	Ile	Thr	Leu	Lys	Pro	Glu	Gln	Ile	Ala	Glu	Leu	Glu
			325						330					335	
Thr	Pro	Tyr	Lys	Pro	His	Pro	Val	Val	Gly	Phe	Lys				
	340						345								

<210> 5

<211> 398

<212> PRT

<213> Escherichia coli

<400> 5

Met	Lys	Gln	Leu	Thr	Ile	Leu	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Cys	Ser
1				5					10					15	

Thr	Leu	Asp	Val	Val	Arg	His	Asn	Pro	Glu	His	Phe	Arg	Val	Val	Ala
		20						25					30		

Leu Val Ala Gly Lys Asn Val Thr Arg Met Val Glu Gln Cys Leu Glu

35

40

45

Phe Ser Pro Arg Tyr Ala Val Met Asp Asp Glu Ala Ser Ala Lys Leu

50

55

60

Leu Lys Thr Met Leu Gln Gln Gln Gly Ser Arg Thr Glu Val Leu Ser

65

70

75

80

Gly Gln Gln Ala Ala Cys Asp Met Ala Ala Leu Glu Asp Val Asp Gln

85

90

95

Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu Ala

100

105

110

Ala Ile Arg Ala Gly Lys Thr Ile Leu Leu Ala Asn Lys Glu Ser Leu

115

120

125

Val Thr Cys Gly Arg Leu Phe Met Asp Ala Val Lys Gln Ser Lys Ala

130

135

140

Gln Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln Ser Leu

145

150

155

160

Pro Gln Pro Ile Gln His Asn Leu Gly Tyr Ala Asp Leu Glu Gln Asn

165

170

175

Gly Val Val Ser Ile Leu Leu Thr Gly Ser Gly Gly Pro Phe Arg Glu

180

185

190

Thr Pro Leu Arg Asp Leu Ala Thr Met Thr Pro Asp Gln Ala Cys Arg

195	200	205
His Pro Asn Trp Ser Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr		
210	215	220
Met Met Asn Lys Gly Leu Glu Tyr Ile Glu Ala Arg Trp Leu Phe Asn		
225	230	235 240
Ala Ser Ala Ser Gln Met Glu Val Leu Ile His Pro Gln Ser Val Ile		
245	250	255
His Ser Met Val Arg Tyr Gln Asp Gly Ser Val Leu Ala Gln Leu Gly		
260	265	270
Glu Pro Asp Met Val Arg Gln Leu Pro Thr Pro Trp Ala Trp Pro Asn		
275	280	285
Arg Val Asn Ser Gly Val Lys Pro Leu Asp Phe Cys Lys Leu Ser Ala		
290	295	300
Leu Thr Phe Ala Ala Pro Asp Tyr Asp Arg Tyr Pro Cys Leu Lys Leu		
305	310	315 320
Ala Met Glu Ala Phe Glu Gln Gly Gln Ala Ala Thr Thr Ala Leu Asn		
325	330	335
Ala Ala Asn Glu Ile Thr Val Ala Ala Phe Leu Ala Gln Gln Ile Arg		
340	345	350
Phe Thr Asp Ile Ala Ala Leu Asn Leu Ser Val Leu Glu Lys Met Asp		
355	360	365

Met Arg Glu Pro Gln Cys Val Asp Asp Val Leu Ser Val Asp Ala Asn
 370 375 380

Ala Arg Glu Val Ala Arg Lys Glu Val Met Arg Leu Ala Ser
 385 390 395

<210> 6

<211> 1860

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1).. (1860)

<400> 6

atg agt ttt gat att gcc aaa tac ccg acc ctg gca ctg gtc gac tcc 48

Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
 1 5 10 15

acc cag gag tta cga ctg ttg ccg aaa gag agt tta ccg aaa ctc tgc 96

Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
 20 25 30

gac gaa ctg cgc cgc tat tta ctc gac agc gtg agc cgt tcc agc ggg 144

Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
 35 40 45

cac ttc gcc tcc ggg ctg ggc acg gtc gaa ctg acc gtg gcg ctg cac 192

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His

50

55

60

tat gtc tac aac acc ccg ttt gac caa ttg att tgg gat gtg ggg cat 240

Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His

65

70

75

80

cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc 288

Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly

85

90

95

acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa 336

Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu

100

105

110

agc gaa tat gac gta tta agc gtc ggg cat tca tca acc tcc atc agt 384

Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser

115

120

125

gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc 432

Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg

130

135

140

cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcg 480

Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala

145	150	155	160	
ttt gaa gcg atg aat cac gcg ggc gat atc cgt cct gat atg ctg gtg	528			
Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val				
165	170	175		
att ctc aac gac aat gaa atg tcg att tcc gaa aat gtc ggc gcg ctc	576			
Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu				
180	185	190		
aac aac cat ctg gca cag ctg ctt tcc ggt aag ctt tac tct tca ctg	624			
Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu				
195	200	205		
cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccg cca att aaa gag	672			
Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu				
210	215	220		
ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc	720			
Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly				
225	230	235	240	
acg ttg ttt gaa gag ctg ggc ttt aac tac atc ggc ccg gtg gac ggt	768			
Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly				
245	250	255		
cac gat gtg ctg ggg ctt atc acc acg cta aag aac atg cgc gac ctg	816			

His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu	
260 265 270	
aaa ggc ccg cag ttc ctg cat atc atg acc aaa aaa ggt cgt ggt tat	864
Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr	
275 280 285	
gaa ccg gca gaa aaa gac ccg atc act ttc cac gcc gtg cct aaa ttt	912
Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe	
290 295 300	
gat ccc tcc agc ggt tgt ttg ccg aaa agt agc ggc ggt ttg ccg agc	960
Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser	
305 310 315 320	
tat tca aaa atc ttt ggc gac tgg ttg tgc gaa acg gca gcg aaa gac	1008
Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp	
325 330 335	
aac aag ctg atg gcg att act ccg gcg atg cgt gaa ggt tcc ggc atg	1056
Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met	
340 345 350	
gtc gag ttt tca cgt aaa ttc ccg gat cgc tac ttc gac gtg gca att	1104
Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile	
355 360 365	

gcc gag caa cac gcg gtg acc ttt gct gcg ggt ctg gcg att ggt ggg 1152

Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
370 375 380

tac aaa ccc att gtc gcg att tac tcc act ttc ctg caa cgc gcc tat 1200

Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
385 390 395 400

gat cag gtg ctg cat gac gtg gcg att caa aag ctt ccg gtc ctg ttc 1248

Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
405 410 415

gcc atc gac cgc gcg ggc att gtt ggt gct gac ggt caa acc cat cag 1296

Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
420 425 430

ggt gct ttt gat ctc tct tac ctg cgc tgc ata ccg gaa atg gtc att 1344

Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
435 440 445

atg acc ccg agc gat gaa aac gaa tgt cgc cag atg ctc tat acc ggc 1392

Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
450 455 460

tat cac tat aac gat ggc ccg tca gcg gtg cgc tac ccg cgt ggc aac 1440

cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att 1776

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile

580

585

590

ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc 1824

Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala

595

600

605

gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca 1860

Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala

610

615

620

<210> 7

<211> 897

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1).. (897)

<400> 7

atg gac ttt ccg cag caa ctc gaa gcc tgc gtt aag cag gcc aac cag 48

Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln

1

5

10

15

gcg ctg agc cgt ttt atc gcc cca ctg ccc ttt cag aac act ccc gtg 96

Ala	Leu	Ser	Arg	Phe	Ile	Ala	Pro	Leu	Pro	Phe	Gln	Asn	Thr	Pro	Val	
			20					25						30		
gtc	gaa	acc	atg	cag	tat	ggc	gca	tta	tta	ggg	ggg	aag	cgc	ctg	cga	144
Val	Glu	Thr	Met	Gln	Tyr	Gly	Ala	Leu	Leu	Gly	Gly	Lys	Arg	Leu	Arg	
			35					40						45		
cct	ttc	ctg	gtt	tat	gcc	acc	ggg	cat	atg	ttc	ggc	gtt	agc	aca	aac	192
Pro	Phe	Leu	Val	Tyr	Ala	Thr	Gly	His	Met	Phe	Gly	Val	Ser	Thr	Asn	
			50					55						60		
acg	ctg	gac	gca	ccc	gct	gcc	gcc	gtt	gag	tgt	atc	cac	gct	tac	tca	240
Thr	Leu	Asp	Ala	Pro	Ala	Ala	Ala	Val	Glu	Cys	Ile	His	Ala	Tyr	Ser	
			65					70						75		80
tta	att	cat	gat	gat	tta	ccg	gca	atg	gat	gat	gac	gat	ctg	cgt	cgc	288
Leu	Ile	His	Asp	Asp	Leu	Pro	Ala	Met	Asp	Asp	Asp	Asp	Leu	Arg	Arg	
								85						90		95
ggg	ttg	cca	acc	tgc	cat	gtg	aag	ttt	ggc	gaa	gca	aac	gcg	att	ctc	336
Gly	Leu	Pro	Thr	Cys	His	Val	Lys	Phe	Gly	Glu	Ala	Asn	Ala	Ile	Leu	
								100						105		110
gct	ggc	gac	gct	tta	caa	acg	ctg	gcg	ttc	tcg	att	tta	agc	gat	gcc	384
Ala	Gly	Asp	Ala	Leu	Gln	Thr	Leu	Ala	Phe	Ser	Ile	Leu	Ser	Asp	Ala	
								115						120		125

gat atg ccg gaa gtg tcg gac cgc gac aga att tcg atg att tct gaa 432

Asp Met Pro Glu Val Ser Asp Arg Asp Arg Ile Ser Met Ile Ser Glu

130

135

140

ctg gcg agc gcc agt ggt att gcc gga atg tgc ggt ggt cag gca tta 480

Leu Ala Ser Ala Ser Gly Ile Ala Gly Met Cys Gly Gly Gln Ala Leu

145

150

155

160

gat tta gac gcg gaa ggc aaa cac gta cct ctg gac gcg ctt gag cgt 528

Asp Leu Asp Ala Glu Gly Lys His Val Pro Leu Asp Ala Leu Glu Arg

165

170

175

att cat cgt cat aaa acc ggc gca ttg att cgc gcc gcc gtt cgc ctt 576

Ile His Arg His Lys Thr Gly Ala Leu Ile Arg Ala Ala Val Arg Leu

180

185

190

ggt gca tta agc gcc gga gat aaa gga cgt cgt gct ctg ccg gta ctc 624

Gly Ala Leu Ser Ala Gly Asp Lys Gly Arg Arg Ala Leu Pro Val Leu

195

200

205

gac aag tat gca gag agc atc ggc ctt gcc ttc cag gtt cag gat gac 672

Asp Lys Tyr Ala Glu Ser Ile Gly Leu Ala Phe Gln Val Gln Asp Asp

210

215

220

atc ctg gat gtg gtg gga gat act gca acg ttg gga aaa cgc cag ggt 720

Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly

225	230	235	240	
gcc gac cag caa ctt ggt aaa agt acc tac cct gca ctt ctg ggt ctt				768
Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu				
	245	250	255	
gag caa gcc cgg aag aaa gcc cgg gat ctg atc gac gat gcc cgt cag				816
Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln				
	260	265	270	
tcg ctg aaa caa ctg gct gaa cag tca ctc gat acc tcg gca ctg gaa				864
Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu				
	275	280	285	
gcg cta gcg gac tac atc atc cag cgt aat aaa				897
Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys				
	290	295		

<210> 8

<211> 240

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1).. (240)

<400> 8

atg ccg aag aaa aat gag gcg ccc gcc agc ttt gaa aag gcg ctg agc 48

Met Pro Lys Lys Asn Glu Ala Pro Ala Ser Phe Glu Lys Ala Leu Ser

1

5

10

15

gag ctg gaa cag att gta acc cgt ctg gaa agt ggc gac ctg ccg ctg 96

Glu Leu Glu Gln Ile Val Thr Arg Leu Glu Ser Gly Asp Leu Pro Leu

20

25

30

gaa gag gcg ctg aac gag ttc gaa cgc ggc gtg cag ctg gca cgt cag 144

Glu Glu Ala Leu Asn Glu Phe Glu Arg Gly Val Gln Leu Ala Arg Gln

35

40

45

ggg cag gcc aaa tta caa caa gcc gaa cag cgc gta caa att ctg ctg 192

Gly Gln Ala Lys Leu Gln Gln Ala Glu Gln Arg Val Gln Ile Leu Leu

50

55

60

tct gac aat gaa gac gcc tct cta acc cct ttt aca ccg gac aat gag 240

Ser Asp Asn Glu Asp Ala Ser Leu Thr Pro Phe Thr Pro Asp Asn Glu

65

70

75

80

<210> 9

<211> 1044

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1).. (1044)

<400> 9

gtg act ggg gtg aac gaa tgc agc cgc agc aca tgc aac ttg aag tat 48

Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr Cys Asn Leu Lys Tyr

1 5 10 15

gac gag tat agc agg agt ggc agc atg caa tac aac ccc tta gga aaa 96

Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr Asn Pro Leu Gly Lys

20 25 30

acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc tgt atg acc ttt ggc 144

Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly Cys Met Thr Phe Gly

35 40 45

gag cca gat cgc ggt aat cac gca tgg aca ctg ccg gaa gaa agc agc 192

Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu Pro Glu Glu Ser Ser

50 55 60

cgt ccc ata att aaa cgt gca ctg gaa ggc ggc ata aat ttc ttt gat 240

Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly Ile Asn Phe Phe Asp

65 70 75 80

acc gcc aac agt tat tct gac ggc agc agc gaa gag atc gtc ggt cgc 288

Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu Glu Ile Val Gly Arg

85 90 95

gca ctg cgg gat ttc gcc cgt cgt gaa gac gtg gtc gtt gcg acc aaa 336

Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val Val Val Ala Thr Lys

100

105

110

gtg ttc cat cgc gtt ggt gat tta ccg gaa gga tta tcc cgt gcg caa 384

Val Phe His Arg Val Gly Asp Leu Pro Glu Gly Leu Ser Arg Ala Gln

115

120

125

att ttg cgc tct atc gac gac agc ctg cga cgt ctc ggc atg gat tat 432

Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg Leu Gly Met Asp Tyr

130

135

140

gtc gat atc ctg caa att cat cgc tgg gat tac aac acg ccg atc gaa 480

Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr Asn Thr Pro Ile Glu

145

150

155

160

gag acg ctg gaa gcc ctc aac gac gtg gta aaa gcc ggg aaa gcg cgt 528

Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys Ala Gly Lys Ala Arg

165

170

175

tat atc ggc gcg tca tca atg cac gct tcg cag ttt gct cag gca ctg 576

Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln Phe Ala Gln Ala Leu

180

185

190

gaa ctc caa aaa cag cac ggc tgg gcg cag ttt gtc agt atg cag gat 624

Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe Val Ser Met Gln Asp

195	200	205	
cac tac aat ctg att tat cgt gaa gaa gag cgc gag atg cta cca ctg	672		
His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg Glu Met Leu Pro Leu			
210	215	220	
tgt tat cag gag ggc gtg gcg gta att cca tgg agc ccg ctg gca agg	720		
Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp Ser Pro Leu Ala Arg			
225	230	235	240
ggc cgt ctg acg cgt ccg tgg gga gaa act acc gca cga ctg gtg tct	768		
Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr Ala Arg Leu Val Ser			
	245	250	255
gat gag gtg ggg aaa aat ctc tat aaa gaa agc gat gaa aat gac gcg	816		
Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser Asp Glu Asn Asp Ala			
	260	265	270
cag atc gca gag cgg tta aca ggc gtc agt gaa gaa ctg ggg gcg aca	864		
Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu Glu Leu Gly Ala Thr			
	275	280	285
cga gca caa gtt gcg ctg gcc tgg ttg ttg agt aaa ccg ggc att gcc	912		
Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser Lys Pro Gly Ile Ala			
	290	295	300
gca ccg att atc gga act tcg cgc gaa gaa cag ctt gat gag cta ttg	960		

Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln Leu Asp Glu Leu Leu

305 310 315 320

aac gcg gtg gat atc act ttg aag ccg gaa cag att gcc gaa ctg gaa 1008

Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln Ile Ala Glu Leu Glu

325 330 335

acg ccg tat aaa ccg cat cct gtc gta gga ttt aaa 1044

Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe Lys

340 345

<210> 10

<211> 1194

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1).. (1194)

<400> 10

atg aag caa ctc acc att ctg ggc tcg acc ggc tcg att ggt tgc agc 48

Met Lys Gln Leu Thr Ile Leu Gly Ser Thr Gly Ser Ile Gly Cys Ser

1 5 10 15

acg ctg gac gtg gtg cgc cat aat ccc gaa cac ttc cgc gta gtt gcg 96

Thr Leu Asp Val Val Arg His Asn Pro Glu His Phe Arg Val Val Ala

20

25

30

ctg gtg gca ggc aaa aat gtc act cgc atg gta gaa cag tgc ctg gaa 144

Leu Val Ala Gly Lys Asn Val Thr Arg Met Val Glu Gln Cys Leu Glu

35

40

45

ttc tct ccc cgc tat gcc gta atg gac gat gaa gcg agt gcg aaa ctt 192

Phe Ser Pro Arg Tyr Ala Val Met Asp Asp Glu Ala Ser Ala Lys Leu

50

55

60

ctt aaa acg atg cta cag caa cag ggt agc cgc acc gaa gtc tta agt 240

Leu Lys Thr Met Leu Gln Gln Gln Gly Ser Arg Thr Glu Val Leu Ser

65

70

75

80

ggg caa caa gcc gct tgc gat atg gca gcg ctt gag gat gtt gat cag 288

Gly Gln Gln Ala Ala Cys Asp Met Ala Ala Leu Glu Asp Val Asp Gln

85

90

95

gtg atg gca gcc att gtt ggc gct gct ggg ctg tta cct acg ctt gct 336

Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu Ala

100

105

110

gcg atc cgc gcg ggt aaa acc att ttg ctg gcc aat aaa gaa tca ctg 384

Ala Ile Arg Ala Gly Lys Thr Ile Leu Leu Ala Asn Lys Glu Ser Leu

115

120

125

gtt acc tgc gga cgt ctg ttt atg gac gcc gta aag cag agc aaa gcg 432

Val Thr Cys Gly Arg Leu Phe Met Asp Ala Val Lys Gln Ser Lys Ala	
130 135 140	
caa ttg tta ccg gtc gat agc gaa cat aac gcc att ttt cag agt tta	480
Gln Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln Ser Leu	
145 150 155 160	
ccg caa cct atc cag cat aat ctg gga tac gct gac ctt gag caa aat	528
Pro Gln Pro Ile Gln His Asn Leu Gly Tyr Ala Asp Leu Glu Gln Asn	
165 170 175	
ggc gtg gtg tcc att tta ctt acc ggg tct ggt ggc cct ttc cgt gag	576
Gly Val Val Ser Ile Leu Leu Thr Gly Ser Gly Gly Pro Phe Arg Glu	
180 185 190	
acg cca ttg cgc gat ttg gca aca atg acg ccg gat caa gcc tgc cgt	624
Thr Pro Leu Arg Asp Leu Ala Thr Met Thr Pro Asp Gln Ala Cys Arg	
195 200 205	
cat ccg aac tgg tgc atg ggg cgt aaa att tct gtc gat tgc gct acc	672
His Pro Asn Trp Ser Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr	
210 215 220	
atg atg aac aaa ggt ctg gaa tac att gaa gcg cgt tgg ctg ttt aac	720
Met Met Asn Lys Gly Leu Glu Tyr Ile Glu Ala Arg Trp Leu Phe Asn	
225 230 235 240	

gcc agc gcc agc cag atg gaa gtg ctg att cac ccg cag tca gtg att 768
Ala Ser Ala Ser Gln Met Glu Val Leu Ile His Pro Gln Ser Val Ile
245 250 255
cac tca atg gtg cgc tat cag gac ggc agt gtt ctg gcg cag ctg ggg 816
His Ser Met Val Arg Tyr Gln Asp Gly Ser Val Leu Ala Gln Leu Gly
260 265 270
gaa ccg gat atg gta cgc caa ttg ccc aca cca tgg gca tgg ccg aat 864
Glu Pro Asp Met Val Arg Gln Leu Pro Thr Pro Trp Ala Trp Pro Asn
275 280 285
cgc gtg aac tct ggc gtg aag ccg ctc gat ttt tgc aaa cta agt gcg 912
Arg Val Asn Ser Gly Val Lys Pro Leu Asp Phe Cys Lys Leu Ser Ala
290 295 300
ttg aca ttt gcc gca ccg gat tat gat cgt tat cca tgc ctg aaa ctg 960
Leu Thr Phe Ala Ala Pro Asp Tyr Asp Arg Tyr Pro Cys Leu Lys Leu
305 310 315 320
gcg atg gag gcg ttc gaa caa ggc cag gca gcg acg aca gca ttg aat 1008
Ala Met Glu Ala Phe Glu Gln Gly Gln Ala Ala Thr Thr Ala Leu Asn
325 330 335
gcc gca aac gaa atc acc gtt gct gct ttt ctt gcg caa caa atc cgc 1056
Ala Ala Asn Glu Ile Thr Val Ala Ala Phe Leu Ala Gln Gln Ile Arg

340	345	350	
ttt acg gat atc gct gcg ttg aat tta tcc gta ctg gaa aaa atg gat			1104
Phe Thr Asp Ile Ala Ala Leu Asn Leu Ser Val Leu Glu Lys Met Asp			
355	360	365	
atg cgc gaa cca caa tgt gtg gac gat gtg tta tct gtt gat gcg aac			1152
Met Arg Glu Pro Gln Cys Val Asp Asp Val Leu Ser Val Asp Ala Asn			
370	375	380	
gcg cgt gaa gtc gcc aga aaa gag gtg atg cgt ctc gca agc			1194
Ala Arg Glu Val Ala Arg Lys Glu Val Met Arg Leu Ala Ser			
385	390	395	

<210> 11

<211> 4390

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (208).. (447)

<220>

<221> CDS

<222> (450).. (1346)

<220>

<221> CDS

<222> (1374).. (3233)

<220>

<221> CDS

<222> (3344).. (4390)

<400> 11

atggcggcaa tggttcgttg gcaagcctta agcgacttgt atagggaaaa atacagcagc 60

ccacacctgc ggctgcatcc aggcgcggaa gtataccact aacatcgctt tgctgtgcac 120

atcaccttac cattgcgcgt tatttgctat ttgccctgag tccgttacca tgacggggcg 180

aaaaatatig agagtcagac attcatt atg ccg aag aaa aat gag gcg ccc gcc 234

Met Pro Lys Lys Asn Glu Ala Pro Ala

1

5

agc ttt gaa aag gcg ctg agc gag ctg gaa cag att gta acc cgt ctg 282

Ser Phe Glu Lys Ala Leu Ser Glu Leu Glu Gln Ile Val Thr Arg Leu

10

15

20

25

gaa agt ggc gac ctg ccg ctg gaa gag gcg ctg aac gag ttc gaa cgc 330

Glu Ser Gly Asp Leu Pro Leu Glu Glu Ala Leu Asn Glu Phe Glu Arg

30

35

40

ggc gtg cag ctg gca cgt cag ggg cag gcc aaa tta caa caa gcc gaa 378

Gly Val Gln Leu Ala Arg Gln Gly Gln Ala Lys Leu Gln Gln Ala Glu	
45 50 55	
cag cgc gta caa att ctg ctg tct gac aat gaa gac gcc tct cta acc	426
Gln Arg Val Gln Ile Leu Leu Ser Asp Asn Glu Asp Ala Ser Leu Thr	
60 65 70	
cct ttt aca ccg gac aat gag ta atg gac ttt ccg cag caa ctc gaa	473
Pro Phe Thr Pro Asp Asn Glu Met Asp Phe Pro Gln Gln Leu Glu	
75 80 1 5	
gcc tgc gtt aag cag gcc aac cag gcg ctg agc cgt ttt atc gcc cca	521
Ala Cys Val Lys Gln Ala Asn Gln Ala Leu Ser Arg Phe Ile Ala Pro	
10 15 20	
ctg ccc ttt cag aac act ccc gtg gtc gaa acc atg cag tat ggc gca	569
Leu Pro Phe Gln Asn Thr Pro Val Val Glu Thr Met Gln Tyr Gly Ala	
25 30 35 40	
tta tta ggt ggt aag cgc ctg cga cct ttc ctg gtt tat gcc acc ggt	617
Leu Leu Gly Gly Lys Arg Leu Arg Pro Phe Leu Val Tyr Ala Thr Gly	
45 50 55	
cat atg ttc ggc gtt agc aca aac acg ctg gac gca ccc gct gcc gcc	665
His Met Phe Gly Val Ser Thr Asn Thr Leu Asp Ala Pro Ala Ala Ala	
60 65 70	

gtt gag tgt atc cac gct tac tca tta att cat gat gat tta ccg gca	713
Val Glu Cys Ile His Ala Tyr Ser Leu Ile His Asp Asp Leu Pro Ala	
75 80 85	
atg gat gat gac gat ctg cgt cgc ggt ttg cca acc tgc cat gtg aag	761
Met Asp Asp Asp Asp Leu Arg Arg Gly Leu Pro Thr Cys His Val Lys	
90 95 100	
ttt ggc gaa gca aac gcg att ctc gct ggc gac gct tta caa acg ctg	809
Phe Gly Glu Ala Asn Ala Ile Leu Ala Gly Asp Ala Leu Gln Thr Leu	
105 110 115 120	
gcg ttc tcg att tta agc gat gcc gat atg ccg gaa gtg tcg gac cgc	857
Ala Phe Ser Ile Leu Ser Asp Ala Asp Met Pro Glu Val Ser Asp Arg	
125 130 135	
gac aga att tcg atg att tct gaa ctg gcg agc gcc agt ggt att gcc	905
Asp Arg Ile Ser Met Ile Ser Glu Leu Ala Ser Ala Ser Gly Ile Ala	
140 145 150	
gga atg tgc ggt ggt cag gca tta gat tta gac gcg gaa ggc aaa cac	953
Gly Met Cys Gly Gly Gln Ala Leu Asp Leu Asp Ala Glu Gly Lys His	
155 160 165	
gta cct ctg gac gcg ctt gag cgt att cat cgt cat aaa acc ggc gca	1001
Val Pro Leu Asp Ala Leu Glu Arg Ile His Arg His Lys Thr Gly Ala	

170	175	180	
ttg att cgc gcc gcc gtt cgc ctt ggt gca tta agc gcc gga gat aaa	1049		
Leu Ile Arg Ala Ala Val Arg Leu Gly Ala Leu Ser Ala Gly Asp Lys			
185	190	195	200
gga cgt cgt gct ctg ccg gta ctc gac aag tat gca gag agc atc ggc	1097		
Gly Arg Arg Ala Leu Pro Val Leu Asp Lys Tyr Ala Glu Ser Ile Gly			
205	210	215	
ctt gcc ttc cag gtt cag gat gac atc ctg gat gtg gtg gga gat act	1145		
Leu Ala Phe Gln Val Gln Asp Asp Ile Leu Asp Val Val Gly Asp Thr			
220	225	230	
gca acg ttg gga aaa cgc cag ggt gcc gac cag caa ctt ggt aaa agt	1193		
Ala Thr Leu Gly Lys Arg Gln Gly Ala Asp Gln Gln Leu Gly Lys Ser			
235	240	245	
acc tac cct gca ctt ctg ggt ctt gag caa gcc cgg aag aaa gcc cgg	1241		
Thr Tyr Pro Ala Leu Leu Gly Leu Glu Gln Ala Arg Lys Lys Ala Arg			
250	255	260	
gat ctg atc gac gat gcc cgt cag tcg ctg aaa caa ctg gct gaa cag	1289		
Asp Leu Ile Asp Asp Ala Arg Gln Ser Leu Lys Gln Leu Ala Glu Gln			
265	270	275	280
tca ctc gat acc tcg gca ctg gaa gcg cta gcg gac tac atc atc cag	1337		

Ser Leu Asp Thr Ser Ala Leu Glu Ala Leu Ala Asp Tyr Ile Ile Gln

285

290

295

cgt aat aaa taaacaataa gtattaatag gccctg atg agt ttt gat att gcc 1391

Arg Asn Lys

Met Ser Phe Asp Ile Ala

1

5

aaa tac ccg acc ctg gca ctg gtc gac tcc acc cag gag tta cga ctg 1439

Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser Thr Gln Glu Leu Arg Leu

10

15

20

ttg ccg aaa gag agt tta ccg aaa ctc tgc gac gaa ctg cgc cgc tat 1487

Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys Asp Glu Leu Arg Arg Tyr

25

30

35

tta ctc gac agc gtg agc cgt tcc agc ggg cac ttc gcc tcc ggg ctg 1535

Leu Leu Asp Ser Val Ser Arg Ser Ser Gly His Phe Ala Ser Gly Leu

40

45

50

ggc acg gtc gaa ctg acc gtg gcg ctg cac tat gtc tac aac acc ccg 1583

Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr Val Tyr Asn Thr Pro

55

60

65

70

ttt gac caa ttg att tgg gat gtg ggg cat cag gct tat ccg cat aaa 1631

Phe Asp Gln Leu Ile Trp Asp Val Gly His Gln Ala Tyr Pro His Lys

75

80

85

att ttg acc gga cgc cgc gac aaa atc ggc acc atc cgt cag aaa ggc 1679
 Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly Thr Ile Arg Gln Lys Gly
 90 95 100
 ggt ctg cac ccg ttc ccg tgg cgc ggc gaa agc gaa tat gac gta tta 1727
 Gly Leu His Pro Phe Pro Trp Arg Gly Glu Ser Glu Tyr Asp Val Leu
 105 110 115
 agc gtc ggg cat tca tca acc tcc atc agt gcc gga att ggt att gcg 1775
 Ser Val Gly His Ser Ser Thr Ser Ile Ser Ala Gly Ile Gly Ile Ala
 120 125 130
 gtt gct gcc gaa aaa gaa ggc aaa aat cgc cgc acc gtc tgt gtc att 1823
 Val Ala Ala Glu Lys Glu Gly Lys Asn Arg Arg Thr Val Cys Val Ile
 135 140 145 150
 ggc gat ggc gcg att acc gca ggc atg gcg ttt gaa gcg atg aat cac 1871
 Gly Asp Gly Ala Ile Thr Ala Gly Met Ala Phe Glu Ala Met Asn His
 155 160 165
 gcg ggc gat atc cgt cct gat atg ctg gtg att ctc aac gac aat gaa 1919
 Ala Gly Asp Ile Arg Pro Asp Met Leu Val Ile Leu Asn Asp Asn Glu
 170 175 180
 atg tcg att tcc gaa aat gtc ggc gcg ctc aac aac cat ctg gca cag 1967

Met Ser Ile Ser Glu Asn Val Gly Ala Leu Asn Asn His Leu Ala Gln	
185	190
195	
ctg ctt tcc ggt aag ctt tac tct tca ctg cgc gaa ggc ggg aaa aaa	2015
Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu Arg Glu Gly Gly Lys Lys	
200	205
210	
gtt ttc tct ggc gtg ccg cca att aaa gag ctg ctc aaa cgc acc gaa	2063
Val Phe Ser Gly Val Pro Pro Ile Lys Glu Leu Leu Lys Arg Thr Glu	
215	220
225	230
gaa cat att aaa ggc atg gta gtg cct ggc acg ttg ttt gaa gag ctg	2111
Glu His Ile Lys Gly Met Val Val Pro Gly Thr Leu Phe Glu Glu Leu	
235	240
245	
ggc ttt aac tac atc ggc ccg gtg gac ggt cac gat gtg ctg ggc ctt	2159
Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly His Asp Val Leu Gly Leu	
250	255
260	
atc acc acg cta aag aac atg cgc gac ctg aaa ggc ccg cag ttc ctg	2207
Ile Thr Thr Leu Lys Asn Met Arg Asp Leu Lys Gly Pro Gln Phe Leu	
265	270
275	
cat atc atg acc aaa aaa ggt cgt ggt tat gaa ccg gca gaa aaa gac	2255
His Ile Met Thr Lys Lys Gly Arg Gly Tyr Glu Pro Ala Glu Lys Asp	
280	285
290	

ccg atc act ttc cac gcc gtg cct aaa ttt gat ccc tcc agc ggt tgt 2303

Pro Ile Thr Phe His Ala Val Pro Lys Phe Asp Pro Ser Ser Gly Cys
295 300 305 310

ttg ccg aaa agt agc ggc ggt ttg ccg agc tat tca aaa atc ttt ggc 2351

Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser Tyr Ser Lys Ile Phe Gly
315 320 325

gac tgg ttg tgc gaa acg gca gcg aaa gac aac aag ctg atg gcg att 2399

Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp Asn Lys Leu Met Ala Ile
330 335 340

act ccg gcg atg cgt gaa ggt tcc ggc atg gtc gag ttt tca cgt aaa 2447

Thr Pro Ala Met Arg Glu Gly Ser Gly Met Val Glu Phe Ser Arg Lys
345 350 355

ttc ccg gat cgc tac ttc gac gtg gca att gcc gag caa cac gcg gtg 2495

Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile Ala Glu Gln His Ala Val
360 365 370

acc ttt gct gcg ggt ctg gcg att ggt ggg tac aaa ccc att gtc gcg 2543

Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly Tyr Lys Pro Ile Val Ala
375 380 385 390

att tac tcc act ttc ctg caa cgc gcc tat gat cag gtg ctg cat gac 2591

Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln Val Leu His Asp

395	400	405	
gtg gcg att caa aag ctt ccg gtc ctg ttc gcc atc gac cgc gcg ggc			2639
Val Ala Ile Gln Lys Leu Pro Val Leu Phe Ala Ile Asp Arg Ala Gly			
410	415	420	
att gtt ggt gct gac ggt caa acc cat cag ggt gct ttt gat ctc tct			2687
Ile Val Gly Ala Asp Gly Gln Thr His Gln Gly Ala Phe Asp Leu Ser			
425	430	435	
tac ctg cgc tgc ata ccg gaa atg gtc att atg acc ccg agc gat gaa			2735
Tyr Leu Arg Cys Ile Pro Glu Met Val Ile Met Thr Pro Ser Asp Glu			
440	445	450	
aac gaa tgt cgc cag atg ctc tat acc ggc tat cac tat aac gat ggc			2783
Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly Tyr His Tyr Asn Asp Gly			
455	460	465	470
ccg tca gcg gtg cgc tac ccg cgt ggc aac gcg gtc ggc gtg gaa ctg			2831
Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn Ala Val Gly Val Glu Leu			
475	480	485	
acg ccg ctg gaa aaa cta cca att ggc aaa ggc att gtg aag cgt cgt			2879
Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys Gly Ile Val Lys Arg Arg			
490	495	500	
ggc gag aaa ctg gcg atc ctt aac ttt ggt acg ctg atg cca gaa gcg			2927

Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly Thr Leu Met Pro Glu Ala

505

510

515

gcg aaa gtc gcc gaa tcg ctg aac gcc acg ctg gtc gat atg cgt ttt 2975

Ala Lys Val Ala Glu Ser Leu Asn Ala Thr Leu Val Asp Met Arg Phe

520

525

530

gtg aaa ccg ctt gat gaa gcg tta att ctg gaa atg gcc gcc agc cat 3023

Val Lys Pro Leu Asp Glu Ala Leu Ile Leu Glu Met Ala Ala Ser His

535

540

545

550

gaa gcg ctg gtc acc gta gaa gaa aac gcc att atg ggc ggc gca ggc 3071

Glu Ala Leu Val Thr Val Glu Glu Asn Ala Ile Met Gly Gly Ala Gly

555

560

565

agc ggc gtg aac gaa gtg ctg atg gcc cat cgt aaa cca gta ccc gtg 3119

Ser Gly Val Asn Glu Val Leu Met Ala His Arg Lys Pro Val Pro Val

570

575

580

ctg aac att ggc ctg ccg gac ttc ttt att ccg caa gga act cag gaa 3167

Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile Pro Gln Gly Thr Gln Glu

585

590

595

gaa atg cgc gcc gaa ctc ggc ctc gat gcc gct ggt atg gaa gcc aaa 3215

Glu Met Arg Ala Glu Leu Gly Leu Asp Ala Ala Gly Met Glu Ala Lys

600

605

610

atc aag gcc tgg ctg gca taatccctac tccactcctg ctatgcttaa 3263

Ile Lys Ala Trp Leu Ala

615 620

gaaattattc atagactcta aataattcga gttgcaggaa ggcggcaaac gagtgaagcc 3323

ccaggagctt acataagtaa gtg act ggg gtg aac gaa tgc agc cgc agc aca 3376

Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr

1 5 10

tgc aac ttg aag tat gac gag tat agc agg agt ggc agc atg caa tac 3424

Cys Asn Leu Lys Tyr Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr

15 20 25

aac ccc tta gga aaa acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc 3472

Asn Pro Leu Gly Lys Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly

30 35 40

tgt atg acc ttt ggc gag cca gat cgc ggt aat cac gca tgg aca ctg 3520

Cys Met Thr Phe Gly Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu

45 50 55

ccg gaa gaa agc agc cgt ccc ata att aaa cgt gca ctg gaa ggc ggc 3568

Pro Glu Glu Ser Ser Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly

60 65 70 75

ata aat ttc ttt gat acc gcc aac agt tat tct gac ggc agc agc gaa 3616

Ile Asn Phe Phe Asp Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu
80 85 90

gag atc gtc ggt cgc gca ctg cgg gat ttc gcc cgt cgt gaa gac gtg 3664

Glu Ile Val Gly Arg Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val
95 100 105

gtc gtt gcg acc aaa gtg ttc cat cgc gtt ggt gat tta ccg gaa gga 3712

Val Val Ala Thr Lys Val Phe His Arg Val Gly Asp Leu Pro Glu Gly
110 115 120

tta tcc cgt gcg caa att ttg cgc tct atc gac gac agc ctg cga cgt 3760

Leu Ser Arg Ala Gln Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg
125 130 135

ctc ggc atg gat tat gtc gat atc ctg caa att cat cgc tgg gat tac 3808

Leu Gly Met Asp Tyr Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr
140 145 150 155

aac acg ccg atc gaa gag acg ctg gaa gcc ctc aac gac gtg gta aaa 3856

Asn Thr Pro Ile Glu Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys
160 165 170

gcc ggg aaa gcg cgt tat atc ggc gcg tca tca atg cac gct tcg cag 3904

Ala Gly Lys Ala Arg Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln
175 180 185

ttt gct cag gca ctg gaa ctc caa aaa cag cac ggc tgg gcg cag ttt 3952

Phe Ala Gln Ala Leu Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe
190 195 200

gtc agt atg cag gat cac tac aat ctg att tat cgt gaa gaa gag cgc 4000

Val Ser Met Gln Asp His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg
205 210 215

gag atg cta cca ctg tgt tat cag gag ggc gtg gcg gta att cca tgg 4048

Glu Met Leu Pro Leu Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp
220 225 230 235

agc ccg ctg gca agg ggc cgt ctg acg cgt ccg tgg gga gaa act acc 4096

Ser Pro Leu Ala Arg Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr
240 245 250

gca cga ctg gtg tct gat gag gtg ggg aaa aat ctc tat aaa gaa agc 4144

Ala Arg Leu Val Ser Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser
255 260 265

gat gaa aat gac gcg cag atc gca gag cgg tta aca ggc gtc agt gaa 4192

Asp Glu Asn Asp Ala Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu
270 275 280

gaa ctg ggg gcg aca cga gca caa gtt gcg ctg gcc tgg ttg ttg agt 4240

Glu Leu Gly Ala Thr Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser
 285 290 295

aaa ccg ggc att gcc gca ccg att atc gga act tcg cgc gaa gaa cag 4288

Lys Pro Gly Ile Ala Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln
 300 305 310 315

ctt gat gag cta ttg aac gcg gtg gat atc act ttg aag ccg gaa cag 4336

Leu Asp Glu Leu Leu Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln
 320 325 330

att gcc gaa ctg gaa acg ccg tat aaa ccg cat cct gtc gta gga ttt 4384

Ile Ala Glu Leu Glu Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe
 335 340 345

aaa taa 4390

Lys

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 12

ccggatccat ggcggcaatg gticgttggc aag 33

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 13

ccgaattc ttt atttaa atcc tacgacagga tgcg

34

<210> 14

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 14

ccggatccat gagttttgat attgccaaat acc

33

<210> 15

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 15

ccgaattctt atgccagcca ggccttgatt ttg

33

<210> 16

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 16

ccgaattctt actcattgtc cgggtgtaaaa ggg

33

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 17

ccggatccat ggactttccg cagcaactcg aag

33

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 18

ccgaattctt atttattacg ctggatgatg tag

33

<210> 19

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 19

ccggatccta atccctactc cactcctgct atg

33

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 20

gggggatcca agcaactcac cattctgggc

30

<210> 21

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 21

gggggatccg ctgtcgagac gcatcacctc

30

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 22

gggggatcca gttttgatat tgccaaatac cc

32

<210> 23

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 23

gggggatcct gccagccagg ccttgatttt gg

32

<210> 24

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 24

gggggatccg agcaactcac cattctgggc

30

<210> 25

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 25

gggggatccg cttgcgagac gcatcacctc

30

<210> 26

<211> 637

<212> PRT

<213> Rhodobacter sphaeroides

<400> 26

Met Thr Asp Arg Pro Cys Thr Pro Thr Leu Asp Arg Val Thr Leu Pro

1 5 10 15

Val Asp Met Lys Gly Leu Thr Asp Arg Glu Leu Arg Ser Leu Ala Asp

20 25 30

Glu Leu Arg Ala Glu Thr Ile Ser Ala Val Ser Val Thr Gly Gly His

35 40 45

Leu Gly Ala Gly Leu Gly Val Val Glu Leu Thr Val Ala Leu His Ala

50 55 60

Val Phe Asp Ala Pro Arg Asp Lys Ile Ile Trp Asp Val Gly His Gln

65 70 75 80

Cys Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Arg Ile Arg Thr

85 90 95

Leu Arg Gln Gly Gly Gly Leu Ser Gly Phe Thr Lys Arg Ser Glu Ser

100 105 110

Pro Tyr Asp Cys Phe Gly Ala Gly His Ser Ser Thr Ser Ile Ser Ala
115 120 125

Ala Val Gly Phe Ala Ala Ala Arg Glu Met Gly Gly Asp Thr Gly Asp
130 135 140

Ala Val Ala Val Ile Gly Asp Gly Ser Met Ser Ala Gly Met Ala Phe
145 150 155 160

Glu Ala Leu Asn His Gly Gly His Leu Lys Asn Arg Val Ile Val Ile
165 170 175

Leu Asn Asp Asn Glu Met Ser Ile Ala Pro Pro Val Gly Ala Leu Ser
180 185 190

Ser Tyr Leu Ser Arg Leu Tyr Ala Gly Ala Pro Phe Gln Asp Phe Lys
195 200 205

Ala Ala Ala Lys Gly Ala Leu Gly Leu Leu Pro Glu Pro Phe Gln Glu
210 215 220

Gly Ala Arg Arg Ala Lys Glu Met Leu Lys Ser Val Thr Val Gly Gly
225 230 235 240

Thr Leu Phe Glu Glu Leu Gly Phe Ser Tyr Val Gly Pro Ile Asp Gly
245 250 255

His Asp Leu Asp Gln Leu Leu Pro Val Leu Arg Thr Val Lys Gln Arg
260 265 270

Ala His Ala Pro Val Leu Ile His Val Ile Thr Lys Lys Gly Arg Gly

275	280	285
Tyr Ala Pro Ala Glu Ala Ala Arg Asp Arg Gly His Ala Thr Asn Lys		
290	295	300
Phe Asn Val Leu Thr Gly Ala Gln Val Lys Pro Val Ser Asn Ala Pro		
305	310	315 320
Ser Tyr Thr Lys Val Phe Ala Gln Ser Leu Ile Lys Glu Ala Glu Val		
	325	330 335
Asp Glu Arg Ile Cys Ala Val Thr Ala Ala Met Pro Asp Gly Thr Gly		
	340	345 350
Leu Asn Leu Phe Gly Glu Arg Phe Pro Lys Arg Thr Phe Asp Val Gly		
	355	360 365
Ile Ala Glu Gln His Ala Val Thr Phe Ser Ala Ala Leu Ala Ala Gly		
	370	375 380
Gly Met Arg Pro Phe Cys Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly		
385	390	395 400
Tyr Asp Gln Ile Val His Asp Val Ala Ile Gln Arg Leu Pro Val Arg		
	405	410 415
Phe Ala Ile Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Ala Thr His		
	420	425 430
Ala Gly Ser Phe Asp Val Ala Phe Leu Ser Asn Leu Pro Gly Ile Val		
435	440	445

Val Met Ala Ala Ala Asp Glu Ala Glu Leu Val His Met Val Ala Thr
450 455 460

Ala Ala Ala His Asp Glu Gly Pro Ile Ala Phe Arg Tyr Pro Arg Gly
465 470 475 480

Asp Gly Val Gly Val Glu Met Pro Val Lys Gly Val Pro Leu Gln Ile
485 490 495

Gly Arg Gly Arg Val Val Arg Glu Gly Thr Arg Ile Ala Leu Leu Ser
500 505 510

Phe Gly Thr Arg Leu Ala Glu Val Gln Val Ala Ala Glu Ala Leu Arg
515 520 525

Ala Arg Gly Ile Ser Pro Thr Val Ala Asp Ala Arg Phe Ala Lys Pro
530 535 540

Leu Asp Arg Asp Leu Ile Leu Gln Leu Ala Ala His His Glu Ala Leu
545 550 555 560

Ile Thr Ile Glu Glu Gly Ala Ile Gly Gly Phe Gly Ser His Val Ala
565 570 575

Gln Leu Leu Ala Glu Ala Gly Val Phe Asp Arg Gly Phe Arg Tyr Arg
580 585 590

Ser Met Val Leu Pro Asp Thr Phe Ile Asp His Asn Ser Ala Glu Val
595 600 605

Met Tyr Ala Thr Ala Gly Leu Asn Ala Ala Asp Ile Glu Arg Lys Ala
610 615 620

Leu Glu Thr Leu Gly Val Glu Val Leu Ala Arg Arg Ala

625

630

635

<210> 27

<211> 1911

<212> DNA

<213> Rhodobacter sphaeroides

<220>

<221> CDS

<222> (1).. (1911)

<400> 27

atg acc gac aga ccc tgc acg ccg acg ctc gac cgg gtg acg ctc ccg 48

Met Thr Asp Arg Pro Cys Thr Pro Thr Leu Asp Arg Val Thr Leu Pro

1

5

10

15

gtg gac atg aag ggc ctc acg gac cgt gag ctg cgc tcg ctg gcc gac 96

Val Asp Met Lys Gly Leu Thr Asp Arg Glu Leu Arg Ser Leu Ala Asp

20

25

30

gag ctg cgg gcc gaa acg atc tcg gcc gtg tcg gtg acg ggc ggg cat 144

Glu Leu Arg Ala Glu Thr Ile Ser Ala Val Ser Val Thr Gly Gly His

35

40

45

ctg ggc gca ggc ctc ggc gtg gtg gag ttg acg gtt gcg ctg cat gcg 192

Leu Gly Ala Gly Leu Gly Val Val Glu Leu Thr Val Ala Leu His Ala

50

55

60

gtc ttc gat gcg ccg cgc gac aag atc atc tgg gac gtg ggc cac cag 240
 Val Phe Asp Ala Pro Arg Asp Lys Ile Ile Trp Asp Val Gly His Gln
 65 70 75 80

tgc tac ccc cac aag atc ctg acc ggg cgg cgc gac cgc atc cgc aca 288
 Cys Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Arg Ile Arg Thr
 85 90 95

ctg cgg cag ggc ggg ggt ctc tcg ggc ttc acc aag cgc tcc gag agc 336
 Leu Arg Gln Gly Gly Gly Leu Ser Gly Phe Thr Lys Arg Ser Glu Ser
 100 105 110

ccc tac gac tgt ttc ggc gcg ggc cat tcc tcg acc tcg atc tcg gcc 384
 Pro Tyr Asp Cys Phe Gly Ala Gly His Ser Ser Thr Ser Ile Ser Ala
 115 120 125

gcg gtg ggc ttt gcc gcg gcg cgc gag atg ggc ggc gac acg ggc gac 432
 Ala Val Gly Phe Ala Ala Ala Arg Glu Met Gly Gly Asp Thr Gly Asp
 130 135 140

gcg gtg gcg gtg atc ggc gat ggc tcg atg tcg gcc ggc atg gcc ttc 480
 Ala Val Ala Val Ile Gly Asp Gly Ser Met Ser Ala Gly Met Ala Phe
 145 150 155 160

gag gcg ctg aac cac ggc ggg cac ctg aag aac cgg gtg atc gtg atc 528
 Glu Ala Leu Asn His Gly Gly His Leu Lys Asn Arg Val Ile Val Ile
 165 170 175

ctg aac gac aat gag atg agc atc gcg ccg ccg gtg ggg gcg ctg tcg 576
 Leu Asn Asp Asn Glu Met Ser Ile Ala Pro Pro Val Gly Ala Leu Ser

180	185	190	
tcc tat ctc tgc cgg ctc tat gcg ggc gcg ccg ttc cag gac ttc aag	624		
Ser Tyr Leu Ser Arg Leu Tyr Ala Gly Ala Pro Phe Gln Asp Phe Lys			
195	200	205	
gcg gcc gcc aag gga gcg ctc ggg ctt ctg ccc gaa ccg ttc cag gag	672		
Ala Ala Ala Lys Gly Ala Leu Gly Leu Leu Pro Glu Pro Phe Gln Glu			
210	215	220	
ggc gcg cgc cgc gcc aag gag atg ctg aag agc gtc acc gtc ggc ggc	720		
Gly Ala Arg Arg Ala Lys Glu Met Leu Lys Ser Val Thr Val Gly Gly			
225	230	235	240
acg ctc ttc gag gag ctg ggt ttc tcc tat gtc ggc ccg atc gac ggg	768		
Thr Leu Phe Glu Glu Leu Gly Phe Ser Tyr Val Gly Pro Ile Asp Gly			
245	250	255	
cac gat ctc gac cag ctt ctg ccg gtg ctg cgg acc gtc aag cag cgg	816		
His Asp Leu Asp Gln Leu Leu Pro Val Leu Arg Thr Val Lys Gln Arg			
260	265	270	
gcg cat gcg ccg gtg ctg atc cat gtc atc acc aag aag ggc agg ggc	864		
Ala His Ala Pro Val Leu Ile His Val Ile Thr Lys Lys Gly Arg Gly			
275	280	285	
tat gct ccg gcc gag gcc gcg cgc gac cgc ggc cat gcc acg aac aag	912		
Tyr Ala Pro Ala Glu Ala Ala Arg Asp Arg Gly His Ala Thr Asn Lys			
290	295	300	
ttc aac gtc ctg acc ggc gcg cag gtg aag ccg gtc tgc aac gcc ccc	960		

gcg ggc tcg ttc gac gtg gcc ttc ctg tcg aac ctg ccc ggc atc gtg 1344
 Ala Gly Ser Phe Asp Val Ala Phe Leu Ser Asn Leu Pro Gly Ile Val
 435 440 445

gtg atg gcc gcc gcc gac gag gcc gag ctc gtc cat atg gtg gcc acc 1392
 Val Met Ala Ala Ala Asp Glu Ala Glu Leu Val His Met Val Ala Thr
 450 455 460

gcc gcc gcc cat gac gaa ggg ccc atc gcc ttc cgc tac ccg cgc ggc 1440
 Ala Ala Ala His Asp Glu Gly Pro Ile Ala Phe Arg Tyr Pro Arg Gly
 465 470 475 480

gac ggc gtg ggg gtc gag atg ccg gtg aag ggc gtg ccg ctc cag atc 1488
 Asp Gly Val Gly Val Glu Met Pro Val Lys Gly Val Pro Leu Gln Ile
 485 490 495

ggc cgc ggc cgt gtg gtg cgc gag ggc acg cga atc gcg ctt ttg tcc 1536
 Gly Arg Gly Arg Val Val Arg Glu Gly Thr Arg Ile Ala Leu Leu Ser
 500 505 510

ttc ggc acc cgt ctg gcc gag gtg cag gtg gcc gcc gag gcg ctg cgt 1584
 Phe Gly Thr Arg Leu Ala Glu Val Gln Val Ala Ala Glu Ala Leu Arg
 515 520 525

gcg cgc ggg atc tct ccc acg gtt gcg gat gcg cgc ttt gca aag ccg 1632
 Ala Arg Gly Ile Ser Pro Thr Val Ala Asp Ala Arg Phe Ala Lys Pro
 530 535 540

ctc gac cgg gat ctg atc ctg cag ctc gcg gcc cat cac gag gcg ctt 1680
 Leu Asp Arg Asp Leu Ile Leu Gln Leu Ala Ala His His Glu Ala Leu

545	550	555	560	
atc acc atc gag gag ggc gcc atc ggc ggt ttc ggc agc cat gtg gcg				1728
Ile Thr Ile Glu Glu Gly Ala Ile Gly Gly Phe Gly Ser His Val Ala				
	565	570	575	
cag ctt ctg gcc gag gcc ggg gtc ttc gac cgc ggc ttc cgg tat cgc				1776
Gln Leu Leu Ala Glu Ala Gly Val Phe Asp Arg Gly Phe Arg Tyr Arg				
	580	585	590	
tcg atg gtg ctg ccc gac acg ttc atc gac cac aac agc gcg gag gtg				1824
Ser Met Val Leu Pro Asp Thr Phe Ile Asp His Asn Ser Ala Glu Val				
	595	600	605	
atg tat gcc acc gcc ggg ctg aat gcg gcc gac ata gag cgg aag gcg				1872
Met Tyr Ala Thr Ala Gly Leu Asn Ala Ala Asp Ile Glu Arg Lys Ala				
	610	615	620	
ctg gag acg ctg ggg gtg gag gtc ctc gcc cgc cgc gcc				1911
Leu Glu Thr Leu Gly Val Glu Val Leu Ala Arg Arg Ala				
	625	630	635	

<210> 28

<211> 648

<212> PRT

<213> Rhodobacter sphaeroides

<400> 28

Met Thr Asn Pro Thr Pro Arg Pro Glu Thr Pro Leu Leu Asp Arg Val

1

5

10

15

Cys Cys Pro Ala Asp Met Lys Ala Leu Ser Asp Ala Glu Leu Glu Arg
20 25 30

Leu Ala Asp Glu Val Arg Ser Glu Val Ile Ser Val Val Ala Glu Thr
35 40 45

Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala
50 55 60

Leu His Ala Val Phe Asn Thr Pro Thr Asp Lys Leu Val Trp Asp Val
65 70 75 80

Gly His Gln Cys Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Glu Gln
85 90 95

Met Arg Thr Leu Arg Gln Lys Gly Gly Leu Ser Gly Phe Thr Lys Arg
100 105 110

Ser Glu Ser Ala Tyr Asp Pro Phe Gly Ala Ala His Ser Ser Thr Ser
115 120 125

Ile Ser Ala Ala Leu Gly Phe Ala Met Gly Arg Glu Leu Gly Gln Pro
130 135 140

Val Gly Asp Thr Ile Ala Val Ile Gly Asp Gly Ser Ile Thr Ala Gly
145 150 155 160

Met Ala Tyr Glu Ala Leu Asn His Ala Gly His Leu Asn Lys Arg Leu
165 170 175

Phe Val Ile Leu Asn Asp Asn Asp Met Ser Ile Ala Pro Pro Val Gly

180	185	190
Ala Leu Ala Arg Tyr Leu Val Asn Leu Ser Ser Lys Ala Pro Phe Ala		
195	200	205
Thr Leu Arg Ala Ala Ala Asp Gly Leu Glu Ala Ser Leu Pro Gly Pro		
210	215	220
Leu Arg Asp Gly Ala Arg Arg Ala Arg Gln Leu Val Thr Gly Met Pro		
225	230	235 240
Gly Gly Gly Thr Leu Phe Glu Glu Leu Gly Phe Thr Tyr Val Gly Pro		
245	250	255
Ile Asp Gly His Asp Met Glu Ala Leu Leu Gln Thr Leu Arg Ala Ala		
260	265	270
Arg Ala Arg Thr Thr Gly Pro Val Leu Ile His Val Val Thr Lys Lys		
275	280	285
Gly Lys Gly Tyr Ala Pro Ala Glu Asn Ala Pro Asp Lys Tyr His Gly		
290	295	300
Val Asn Lys Phe Asp Pro Val Thr Gly Glu Gln Lys Lys Ser Val Ala		
305	310	315 320
Asn Ala Pro Asn Tyr Thr Lys Val Phe Gly Ser Thr Leu Thr Glu Glu		
325	330	335
Ala Ala Arg Asp Pro Arg Ile Val Ala Ile Thr Ala Ala Met Pro Ser		
340	345	350

Gly Thr Gly Val Asp Ile Met Gln Lys Arg Phe Pro Asn Arg Val Phe
355 360 365

Asp Val Gly Ile Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu
370 375 380

Ala Gly Ala Gly Met Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Leu
385 390 395 400

Gln Arg Gly Tyr Asp Gln Ile Ala His Asp Val Ala Leu Gln Asn Leu
405 410 415

Pro Val Arg Phe Val Ile Asp Arg Ala Gly Leu Val Gly Ala Asp Gly
420 425 430

Ala Thr His Ala Gly Ala Phe Asp Val Gly Phe Leu Thr Ser Leu Pro
435 440 445

Asn Met Thr Val Met Ala Ala Ala Asp Glu Ala Glu Leu Ile His Met
450 455 460

Ile Ala Thr Ala Val Ala Phe Asp Glu Gly Pro Ile Ala Phe Arg Phe
465 470 475 480

Pro Arg Gly Glu Gly Val Gly Val Glu Met Pro Glu Arg Gly Thr Val
485 490 495

Leu Glu Pro Gly Arg Gly Arg Val Val Arg Glu Gly Thr Asp Val Ala
500 505 510

Ile Leu Ser Phe Gly Ala His Leu His Glu Ala Leu Gln Ala Ala Lys
515 520 525

Leu Leu Glu Ala Glu Gly Val Ser Val Thr Val Ala Asp Ala Arg Phe
530 535 540

Ser Arg Pro Leu Asp Thr Gly Leu Ile Asp Gln Leu Val Arg His His
545 550 555 560

Ala Ala Leu Val Thr Val Glu Gln Gly Ala Met Gly Gly Phe Gly Ala
565 570 575

His Val Met His Tyr Leu Ala Asn Ser Gly Gly Phe Asp Gly Gly Leu
580 585 590

Ala Leu Arg Val Met Thr Leu Pro Asp Arg Phe Ile Glu Gln Ala Ser
595 600 605

Pro Glu Asp Met Tyr Ala Asp Ala Gly Leu Arg Ala Glu Asp Ile Ala
610 615 620

Ala Thr Ala Arg Gly Ala Leu Ala Arg Gly Arg Val Met Pro Leu Arg
625 630 635 640

Gln Thr Ala Lys Pro Arg Ala Val
645

<210> 29

<211> 1944

<212> DNA

<213> Rhodobacter sphaeroides

<220>

<221> CDS

<222> (1).. (1944)

<400> 29

atg acc aat ccc acc ccg cga ccc gaa acc ccg ctt ttg gat cgc gtc	48
Met Thr Asn Pro Thr Pro Arg Pro Glu Thr Pro Leu Leu Asp Arg Val	
1 5 10 15	
tgc tgc ccg gcc gac atg aag gcg ctg agt gac gcc gaa ctg gag cgg	96
Cys Cys Pro Ala Asp Met Lys Ala Leu Ser Asp Ala Glu Leu Glu Arg	
20 25 30	
ctg gcc gac gaa gtg cgt tcc gag gtg att tcg gtc gtt gcc gag acg	144
Leu Ala Asp Glu Val Arg Ser Glu Val Ile Ser Val Val Ala Glu Thr	
35 40 45	
gga gga cat ctg ggg tcc tcg ctg ggg gtg gtc gag ctg acc gtc gcg	192
Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala	
50 55 60	
ctg cat gca gtc ttc aac acg ccc acc gac aag ctc gtc tgg gac gtg	240
Leu His Ala Val Phe Asn Thr Pro Thr Asp Lys Leu Val Trp Asp Val	
65 70 75 80	
ggc cac cag tgc tac ccc cac aag atc ctc acc ggc cgg cgc gag cag	288
Gly His Gln Cys Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Glu Gln	
85 90 95	
atg cgc acc ctg cgc cag aag ggc ggc ctc tcg ggc ttc acc aag cgc	336
Met Arg Thr Leu Arg Gln Lys Gly Gly Leu Ser Gly Phe Thr Lys Arg	

100	105	110	
tcg gaa tcc gcc tac gac ccg ttc ggc gcg gcc cat tcc tcg acc tcg			384
Ser Glu Ser Ala Tyr Asp Pro Phe Gly Ala Ala His Ser Ser Thr Ser			
115	120	125	
atc tcg gcc gcg ctc ggc ttt gcc atg ggc cgc gag ctg ggc caa ccc			432
Ile Ser Ala Ala Leu Gly Phe Ala Met Gly Arg Glu Leu Gly Gln Pro			
130	135	140	
gtg ggc gac acg atc gcc gtg atc ggc gac ggc tcg atc acc gcg ggc			480
Val Gly Asp Thr Ile Ala Val Ile Gly Asp Gly Ser Ile Thr Ala Gly			
145	150	155	160
atg gcc tac gag gcg ctg aac cac gcg ggc cat ctg aac aag cgc ctg			528
Met Ala Tyr Glu Ala Leu Asn His Ala Gly His Leu Asn Lys Arg Leu			
165	170	175	
ttc gtg atc ctg aac gac aat gac atg agc atc gcg ccg ccc gtg ggg			576
Phe Val Ile Leu Asn Asp Asn Asp Met Ser Ile Ala Pro Pro Val Gly			
180	185	190	
gct ctg gcg cgc tat ctc gtg aat ctc tcc tcg aag gcg ccc ttc gcc			624
Ala Leu Ala Arg Tyr Leu Val Asn Leu Ser Ser Lys Ala Pro Phe Ala			
195	200	205	
acg ctg cgc gcg gcc gcc gac ggg ctc gag gcc tcg ctg ccg ggg ccg			672
Thr Leu Arg Ala Ala Ala Asp Gly Leu Glu Ala Ser Leu Pro Gly Pro			
210	215	220	
ctc cgc gac ggg gcg cgc cgg gcg cgc cag ctc gtg acc ggg atg ccg			720

ggc acc ggc gtc gac atc atg cag aag cgt ttc ccg aac cgc gtc ttc 1104
 Gly Thr Gly Val Asp Ile Met Gln Lys Arg Phe Pro Asn Arg Val Phe

355

360

365

gac gtg ggc atc gcc gag cag cat gcc gtg acc ttc gcg gcg ggc ctt 1152
 Asp Val Gly Ile Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu

370

375

380

gcc ggg gcc ggg atg aag ccc ttc tgc gcg atc tat tcc tcg ttc ctg 1200
 Ala Gly Ala Gly Met Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Leu
 385 390 395 400

caa cgg ggc tac gac cag atc gcc cat gac gtg gcg ctg cag aac ctt 1248
 Gln Arg Gly Tyr Asp Gln Ile Ala His Asp Val Ala Leu Gln Asn Leu
 405 410 415

ccc gtc cgc ttc gtg atc gac cgg gcg ggg ctc gtg ggg gcc gac ggt 1296
 Pro Val Arg Phe Val Ile Asp Arg Ala Gly Leu Val Gly Ala Asp Gly
 420 425 430

gcg acc cat gcg ggg gcc ttc gat gtg ggc ttc ctc acg tcg ctg ccc 1344
 Ala Thr His Ala Gly Ala Phe Asp Val Gly Phe Leu Thr Ser Leu Pro
 435 440 445

aat atg acc gtg atg gcc gcg gcc gac gag gcc gag ctc atc cac atg 1392
 Asn Met Thr Val Met Ala Ala Ala Asp Glu Ala Glu Leu Ile His Met
 450 455 460

atc gcc acc gcc gtg gcc ttc gac gag ggc ccc att gcc ttc cgc ttc 1440
 Ile Ala Thr Ala Val Ala Phe Asp Glu Gly Pro Ile Ala Phe Arg Phe

465	470	475	480	
ccg cgg ggc gag ggg gtg ggc gtc gag atg ccc gag cgc ggg acc gtg				1488
Pro Arg Gly Glu Gly Val Gly Val Glu Met Pro Glu Arg Gly Thr Val				
	485	490	495	
ctg gaa ccc ggc cgg ggc cgc gtg gtg cgc gag ggg acg gat gtg gcg				1536
Leu Glu Pro Gly Arg Gly Arg Val Val Arg Glu Gly Thr Asp Val Ala				
	500	505	510	
atc ctt tcc ttc ggc gcg cat ctg cac gag gcc ttg cag gcg gcg aaa				1584
Ile Leu Ser Phe Gly Ala His Leu His Glu Ala Leu Gln Ala Ala Lys				
	515	520	525	
ctc ctc gag gcc gag ggg gtg agc gtg acc gtg gcc gac gcc cgc ttc				1632
Leu Leu Glu Ala Glu Gly Val Ser Val Thr Val Ala Asp Ala Arg Phe				
	530	535	540	
tcg cgc ccg ctc gac acg ggg ctc att gac cag ctc gtg cgc cat cac				1680
Ser Arg Pro Leu Asp Thr Gly Leu Ile Asp Gln Leu Val Arg His His				
545	550	555	560	
gcc gcg ctg gtg acg gtg gag cag ggg gcc atg ggc ggc ttc ggc gct				1728
Ala Ala Leu Val Thr Val Glu Gln Gly Ala Met Gly Gly Phe Gly Ala				
	565	570	575	
cat gtc atg cac tat ctc gcc aat tcc ggc ggc ttc gac ggg ggc ctc				1776
His Val Met His Tyr Leu Ala Asn Ser Gly Gly Phe Asp Gly Gly Leu				
	580	585	590	
gcg ctc cgg gtc atg acg ctg ccc gac cgc ttc atc gag cag gcg agc				1824

Ala Leu Arg Val Met Thr Leu Pro Asp Arg Phe Ile Glu Gln Ala Ser
595 600 605

ccc gag gac atg tat gcc gat gcg ggg ctg cgg gcc gag gat atc gcg 1872
Pro Glu Asp Met Tyr Ala Asp Ala Gly Leu Arg Ala Glu Asp Ile Ala
610 615 620

gcc acc gcg cgg ggc gcg ctc gcc cgg ggg cgc gtg atg ccg ctc cgg 1920
Ala Thr Ala Arg Gly Ala Leu Ala Arg Gly Arg Val Met Pro Leu Arg
625 630 635 640

cag acg gca aag ccg cgg gcg gtc 1944
Gln Thr Ala Lys Pro Arg Ala Val
645

<210> 30

<211> 394

<212> PRT

<213> Rhodobacter sphaeroides

<400> 30

Met Arg Ser Leu Ser Ile Phe Gly Ala Thr Gly Ser Ile Gly Glu Ser
1 5 10 15

Thr Phe Asp Leu Val Met Arg Lys Gly Gly Pro Glu Ala Phe Arg Thr
20 25 30

Val Ala Leu Thr Gly Gly Arg Asn Ile Arg Arg Leu Ala Glu Met Ala
35 40 45

Arg Ala Leu Lys Ala Glu Leu Ala Val Thr Ala His Glu Asp Cys Leu
50 55 60

Pro Ala Leu Arg Glu Ala Leu Ala Gly Thr Gly Thr Glu Val Ala Gly
65 70 75 80

Gly Ala Gln Ala Ile Ala Glu Ala Ala Asp Arg Pro Ala Asp Trp Thr
85 90 95

Met Ser Ala Ile Val Gly Ala Ala Gly Leu Val Pro Gly Met Arg Ala
100 105 110

Leu Lys His Gly Arg Thr Leu Ala Leu Ala Asn Lys Glu Ser Leu Val
115 120 125

Thr Ala Gly Gln Leu Leu Met Arg Thr Ala Gln Glu Asn Gly Ala Thr
130 135 140

Ile Leu Pro Val Asp Ser Glu His Ser Ala Val Phe Gln Ala Leu Ala
145 150 155 160

Gly Glu Asp Thr Ala Cys Val Glu Arg Val Ile Ile Thr Ala Ser Gly
165 170 175

Gly Pro Phe Arg Asp Trp Ser Leu Glu Arg Ile Arg Ala Cys Thr Val
180 185 190

Ala Glu Ala Gln Ala His Pro Asn Trp Ser Met Gly Gln Arg Ile Ser
195 200 205

Ile Asp Ser Ala Ser Met Phe Asn Lys Ala Leu Glu Leu Ile Glu Thr
210 215 220

Arg Glu Phe Phe Gly Phe Glu Pro Asp Arg Ile Glu Ala Val Val His
225 230 235 240

Pro Gln Ser Ile Val His Ala Met Val Gly Phe Cys Asp Gly Gly Leu
245 250 255

Met Ala His Leu Gly Pro Ala Asp Met Arg His Ala Ile Gly Phe Ala
260 265 270

Leu Asn Trp Pro Gly Arg Gly Glu Val Pro Val Ala Arg Ile Asp Leu
275 280 285

Ala Gln Ile Ala Ser Leu Thr Phe Gln Lys Pro Asp Glu Glu Arg Phe
290 295 300

Pro Ala Leu Arg Leu Ala Arg Asp Val Met Ala Ala Arg Gly Leu Ser
305 310 315 320

Gly Ala Ala Phe Asn Ala Ala Lys Glu Ile Ala Leu Asp His Phe Ile
325 330 335

Ala Gly Arg Ile Gly Phe Leu Asp Met Ala Ala Val Val Glu Glu Thr
340 345 350

Leu Ala Gly Val Ser Thr Asp Pro Leu Phe Gly Lys Val Pro Asp Ala
355 360 365

Leu Glu Glu Val Leu Ala Met Asp His Leu Ala Arg Arg Ala Ala Glu
370 375 380

Glu Ala Ala Gly Leu Arg Gln Gln Lys Arg

385

390

<210> 31

<211> 1182

<212> DNA

<213> Rhodobacter sphaeroides

<220>

<221> CDS

<222> (1).. (1182)

<400> 31

atg cgc agc ctg tgc atc ttt ggg gcc acc ggc tcc atc ggc gaa tcc 48

Met Arg Ser Leu Ser Ile Phe Gly Ala Thr Gly Ser Ile Gly Glu Ser

1 5 10 15

acc ttc gac ctc gtc atg cgg aag ggc ggg ccc gag gcg ttc cgc acc 96

Thr Phe Asp Leu Val Met Arg Lys Gly Gly Pro Glu Ala Phe Arg Thr

20 25 30

gtc gct ctg acc ggc ggg cgc aac atc cgg cga ctg gcc gaa atg gcg 144

Val Ala Leu Thr Gly Gly Arg Asn Ile Arg Arg Leu Ala Glu Met Ala

35 40 45

cgt gcg ctg aag gcg gag ctt gcc gtc acc gcg cat gag gac tgc ctg 192

Arg Ala Leu Lys Ala Glu Leu Ala Val Thr Ala His Glu Asp Cys Leu

50 55 60

ccc gcg ctg cgc gag gcg ctg gcc ggg acg ggc acc gag gtc gcg ggc 240

Pro Ala Leu Arg Glu Ala Leu Ala Gly Thr Gly Thr Glu Val Ala Gly

65	70	75	80	
ggg gcg cag gcc atc gcc gag gcc gcc gac cgg ccg gcc gac tgg acc				288
Gly Ala Gln Ala Ile Ala Glu Ala Ala Asp Arg Pro Ala Asp Trp Thr				
	85	90	95	
atg tcg gcc atc gtg ggc gcc gcg ggc ctc gtg ccc gga atg cgg gcg				336
Met Ser Ala Ile Val Gly Ala Ala Gly Leu Val Pro Gly Met Arg Ala				
	100	105	110	
ctg aag cac ggc cgc acg ctg gcg ctc gcc aac aag gaa agc ctc gtg				384
Leu Lys His Gly Arg Thr Leu Ala Leu Ala Asn Lys Glu Ser Leu Val				
	115	120	125	
acg gca ggg caa ctc ctg atg cgg acg gcc cag gag aac ggc gcc acg				432
Thr Ala Gly Gln Leu Leu Met Arg Thr Ala Gln Glu Asn Gly Ala Thr				
	130	135	140	
atc ctg ccg gtg gac agc gag cac tcc gcg gtc ttt cag gcg ctg gcg				480
Ile Leu Pro Val Asp Ser Glu His Ser Ala Val Phe Gln Ala Leu Ala				
	145	150	155	160
ggc gag gac acg gcc tgc gtc gag cgc gtc atc atc acg gcg tcc ggc				528
Gly Glu Asp Thr Ala Cys Val Glu Arg Val Ile Ile Thr Ala Ser Gly				
	165	170	175	
ggg ccg ttc cgc gac tgg agc ctc gag cgc atc cgc gcc tgc acc gtg				576
Gly Pro Phe Arg Asp Trp Ser Leu Glu Arg Ile Arg Ala Cys Thr Val				
	180	185	190	
gcc gag gcg cag gcc cat ccc aac tgg tcc atg ggc cag cgg atc tcc				624

Ala Glu Ala Gln Ala His Pro Asn Trp Ser Met Gly Gln Arg Ile Ser	
195	200 205
atc gac agc gcc tcg atg ttc aac aag gcg ctc gag ctg atc gag acg	672
Ile Asp Ser Ala Ser Met Phe Asn Lys Ala Leu Glu Leu Ile Glu Thr	
210	215 220
cgc gaa ttc ttc ggc ttc gag ccg gac cgg atc gag gcg gtc gtc cat	720
Arg Glu Phe Phe Gly Phe Glu Pro Asp Arg Ile Glu Ala Val Val His	
225	230 235 240
ccg caa tcc atc gtc cat gcg atg gtg ggc ttc tgc gac ggg ggc ctg	768
Pro Gln Ser Ile Val His Ala Met Val Gly Phe Cys Asp Gly Gly Leu	
	245 250 255
atg gcc cat ctc ggc ccc gcc gac atg cgc cac gcc atc gga ttc gcg	816
Met Ala His Leu Gly Pro Ala Asp Met Arg His Ala Ile Gly Phe Ala	
	260 265 270
ctg aac tgg ccg ggt cgc ggc gag gtg ccc gtc gcc cgg atc gac ctc	864
Leu Asn Trp Pro Gly Arg Gly Glu Val Pro Val Ala Arg Ile Asp Leu	
	275 280 285
gca cag att gcg agc ctc acc ttc cag aag cct gac gag gaa cgc ttt	912
Ala Gln Ile Ala Ser Leu Thr Phe Gln Lys Pro Asp Glu Glu Arg Phe	
	290 295 300
ccg gcc ctg agg ctt gcg cga gac gtc atg gcg gcg cgc ggc ctg tcg	960
Pro Ala Leu Arg Leu Ala Arg Asp Val Met Ala Ala Arg Gly Leu Ser	
305	310 315 320

ggc gcc gcc ttc aac gcg gcc aag gag atc gcg ctc gat cat ttc atc 1008
 Gly Ala Ala Phe Asn Ala Ala Lys Glu Ile Ala Leu Asp His Phe Ile
 325 330 335

gcc gga cgc atc ggg ttt ctg gac atg gcg gcg gtg gtc gag gag acg 1056
 Ala Gly Arg Ile Gly Phe Leu Asp Met Ala Ala Val Val Glu Glu Thr
 340 345 350

ctc gcg ggc gtt tcg acc gac ccc ctg ttc gga aaa gtg ccc gac gcc 1104
 Leu Ala Gly Val Ser Thr Asp Pro Leu Phe Gly Lys Val Pro Asp Ala
 355 360 365

ctt gag gaa gtg ctg gcc atg gac cat ctc gct cgg aga gcg gca gag 1152
 Leu Glu Glu Val Leu Ala Met Asp His Leu Ala Arg Arg Ala Ala Glu
 370 375 380

gaa gcc gcc ggt ctc cgc cag cag aaa agg 1182
 Glu Ala Ala Gly Leu Arg Gln Gln Lys Arg
 385 390

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 32

aagctgatct gggacgtggg gca

23

<210> 33

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 33

tgctatccgc acaagatcct gac

23

<210> 34

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 34

gcatgctgtt ccgcgatgcc gac

23